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Conservation of human vs. feline genome organization revealed by reciprocal chromosome painting.

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We employed fluorescence in situ hybridization (FISH) with probes established by flow sorting metaphase chromosomes of the domestic cat (*Felis cattus*, 2n = 38) to "paint" homologous segments on human chromosomes and, reciprocally, using human chromosome paints on feline metaphase preparations. The results revealed, by direct microscopic observation, widespread conservation of genome organization between the two mammalian orders and confirmed 90% of the homologous genes mapped to both species. Fourteen of 23 human chromosomes were hybridized with single cat probes, and 9 of 19 cat chromosomes were entirely labeled by a single human probe. All other chromosomes were labeled with only two or, at most, three probes of the respective species. Y-chromosome probes gave no signals. Approximately 30 syntenic segments were identified, and the number of translocations could be estimated to be on the order of one new translocation per 10 million years in the phylogenetic lines leading to human and cat. Using the principle of maximum parsimony, the primitive vs. derived human chromosome segments were identified by comparison to the feline, cattle, and pig genomes, a first step in reconstructing the evolutionary heritage of the mammalian radiations. The results suggest that reciprocal chromosome painting will help reconstruct the history of genomic changes by determining the polarity of chromosomal rearrangements and establishing the ancestral karyotype for each principle branching point in mammalian evolution.

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